

Fig. 1

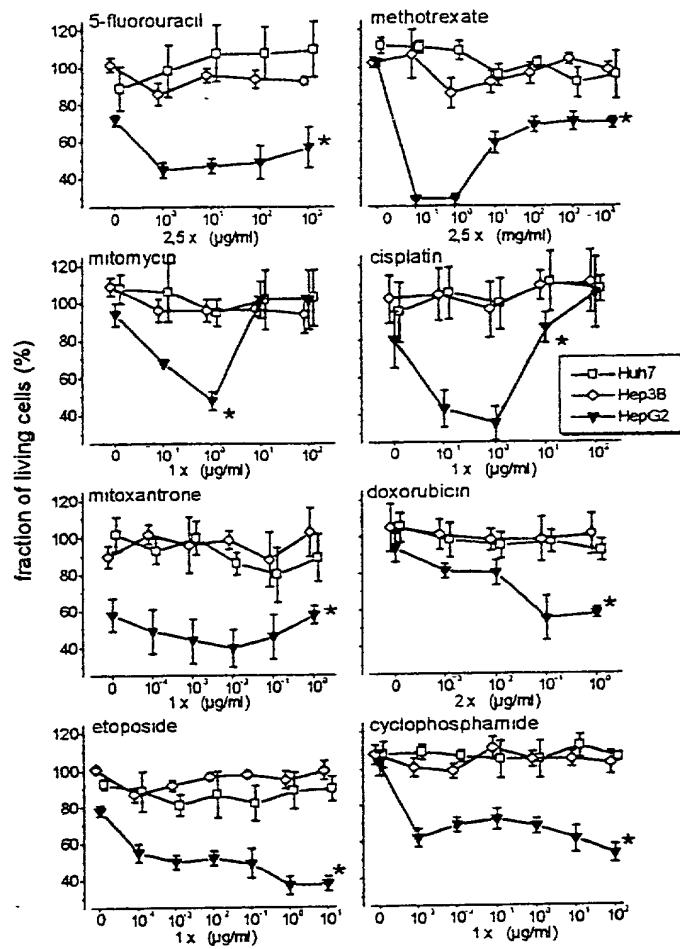


Fig. 2

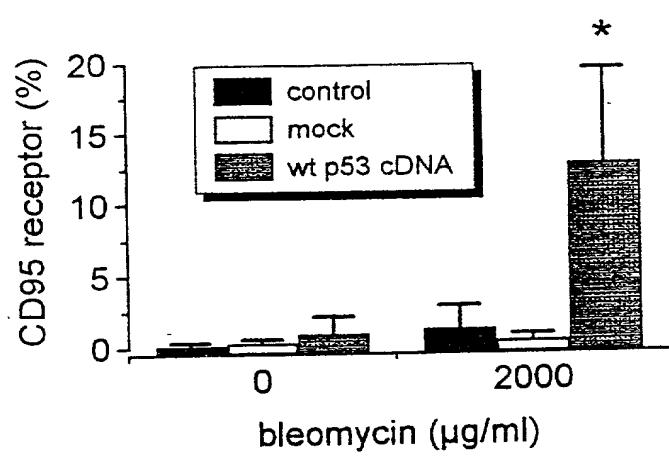


Fig. 3

620 640 660  
GATCCCGCTGGCAGGGGG GCAGCTCGGCGCTCCCTCGG AGACCACTGCGCTCCACGTT  
Sau3A1

680 700 720  
GAGGTGGGCGTGGGGGGCGG ACAGGAATTGAAGCGGAAGT CTGGGAAGCTT~~TAGGGTCGC~~  
HindIII

740 760 780  
TGGAGGGGGACCCGGTTGG AGAGAGGAGCGGAACTCTG GACAAGCCGTGACAAGCCAA  
p63BE

800 820 840  
GCCAAAGGTCCGCTCCGGCG CGGGTGGGTGAGTGCGCGCC GCCCCCGCGGGGGCGGGGAGA

860 GAGCCTGCAGCCTTCAGAAC 880 AGATAT

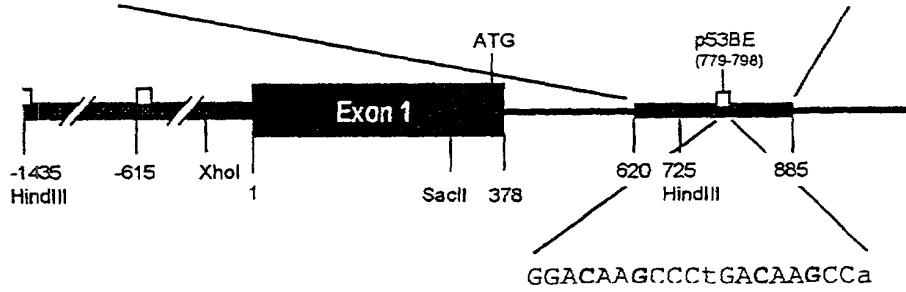


Fig. 4

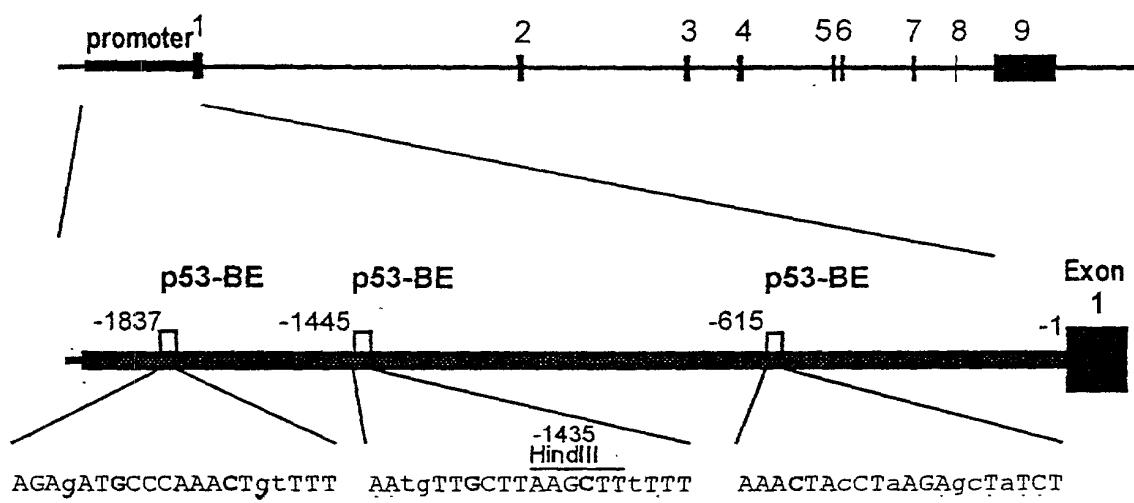


Fig. 5

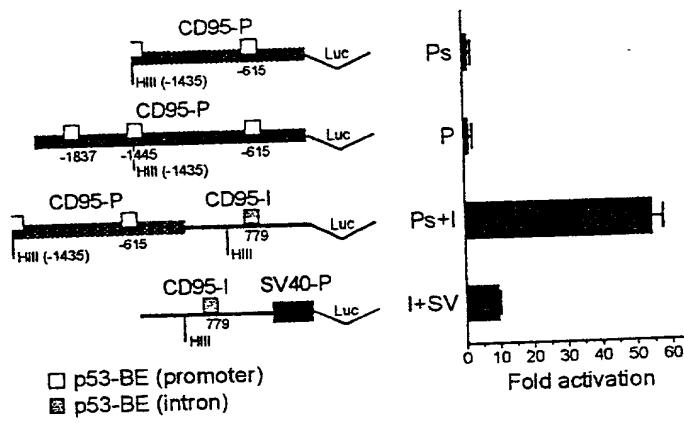


Fig. 6

1 GATCCCGCTGGCAGGCAGGGCAGCTCCGGCGCTCCTCGGAGACCCTGCGCTCCACGTT 60  
1 CTAGGGCGACCCGTCCGCCCGTCGAGGCCGAGGAGCCTCTGGTACGCGAGGTGCAA  
61 GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTAGGGTCGC 120  
61 CTCCACCCGCACCCCCCGCTGTCCCTAACCTCGCCTTCAGACCCCTCGAAATCCCAGCG  
  
<---- 4.P53-BE ---->  
(intron)  
121 TCGAGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAAGCCCTGACAAGCCAA 180  
121 ACCTCCCCCTGGGGCAACCTCTCCTCGCCTTGAGGACCTGTTGGGACTGTTGGTT  
181 GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCAGCGCCGCCCGCGGGGGCGGGGAGA 240  
181 CGGTTCCAGGCGAGGCCGCGCCACCCACTCACGCGGGCGGGCGCCCCGCCCCCTCT  
241 GAGCCTACAGCCTTCAGAACACATATTGCTCATTCTGGCAGTTCTCAGACGTAGGAAA 300  
241 CTCGGATGTCGAAAGTCTTGTATAACGAGTAAAGACCGTCAAGAGTCTGCATCCTT  
301 TAAAGTCAGCACCGAACGAGTGGTTAACCGGGCTCGGAAGAACGGCACCTTCTTT 360  
301 ATTCAAGTCGTGGCTTCGTACCAATTGGCCTCCGAGCCTTCTGGCGTGGAAAAGAAA  
361 CTCGAAAAAGTTATATGGGGCTGAATGAGCTCTGGAGGGCTTACCGTTTTATT 420  
361 GAGCTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAA  
421 GTCACACAGAAAAGGAAACTGCCCTGTCTCCCTCCGGAAATTCTCTCTTTAACGACTGTA 480  
421 CAGTGTGTCTTCCCTTGACGAAACAGAGGGAGGCCCTTAAGAGAGAAATTCTGACAT  
481 AGTCGCTGCCCTGAGTGGTTCTTTGTTCTGCCCTCTCTCTCTCTCTCTCTCT 540  
481 TCAGCGACGGACTACCAAAAGTAAAACAAAACAAAAGACGGGAAGAGAAAGAAGAAAAC  
541 CCCTTCTTAGCTGCACCTCCATGGTATTCTGCTGGTCTCTGCTGGGTTGGTGG 600  
541 GGGAAAGAACGAACTGAGGGTACCAACTAAAGACGAACAGAGGGAGGACGACCCCAACCACC  
601 TACTCGTCCCACCGCACAGAACCCGGCGCTATTATGGCCAAGAAACTTGAGCAGCCT 660  
601 ATGAGCAAGGGTGGCGTGTCTGGCCGCGATAATAACCGGTTCTTGAACTCGTCGGA  
661 GTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAGAGACGTG 720  
661 CAAAACTTCAAGGAGCGAGTCTTACGGTCAACGTCTACCGATTAGTTCTCTGCAC

Fig. 8

2<sup>nd</sup> half of the  
**2.p53-BE**  
 (promoter)

AGCTTTTGGCTACATTTTATTGTAAAG  
 448 -----+-----+-----+-----+ 480  
 TCGAAAAACCGATGTAAAAAAATAAACATTTC

TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAGTAAGGAAGATC  
 481 -----+-----+-----+-----+-----+-----+-----+ 540  
 ATTCAAATTATTAGTAGTGAGTAGTGACCCGATATTACTATTCATAATTCAATTCTTCAG

CACATATGTGAGTTGCTGGCTTATAATTCAACTCAAGAGATACTGATTGTCAATTGT  
 541 -----+-----+-----+-----+-----+-----+-----+ 600  
 GTGTATACTCAACGACCGAATATTAAGTGAGTTCTCTATGACTAAAACAGTTAAC

CCTTCCCCTTTTCTCTTCCCTCCATTCCCTTACCTCTCCTTC  
 601 -----+-----+-----+-----+-----+-----+-----+ 660  
 GGAAAGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGAAATGGAGAGGAAG

CTTCCCTCACACCCCTTCTTCCCTTACATTTTATTTAAATGAACTTT  
 661 -----+-----+-----+-----+-----+-----+-----+ 720  
 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAATAATTACTTGAAAAG

ATTTGGAATAGTTTAGGATTCAAAAATTGCAGAGATAATACAGAGAATGCCATA  
 721 -----+-----+-----+-----+-----+-----+-----+ 780  
 TAAAACCTTATCAAAATCCTAAAGTTTAAACGTCTATTATGTCTTACGGGTAT

TACCATCCTCTTATCCACTTCTTTGTGTCTATTAGATGCTCAGAGTGTGCACAA  
 781 -----+-----+-----+-----+-----+-----+-----+ 840  
 ATGGTAGGAGGAATAGGGTGAAGAAAACACAGATAATCTACGAGTCTCACACACGTGTT

GGCTGGCACGCCAGGGCTTCCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG  
 841 -----+-----+-----+-----+-----+-----+-----+ 900  
 CCGACCGTGGGGTCCAGAAGGAGTACCGTGATTGTCAGATGACTTCCACCTGTCTC

ACAAGCCTATCAACACCTACAAGACTGGTGTAAAGTGCAGTGACAGATGCAAACACAGG  
 901 -----+-----+-----+-----+-----+-----+-----+ 960  
 TGTTCGGATAGTTGTGGATGTTCTGACCACATTACGTCACTGTCTACGTTGTGTC

GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCA  
 991 -----+-----+-----+-----+-----+-----+-----+ 1020  
 CACTACCTTCGGGAGTCCTCCATTGGATGGATCTAAACTCCGGGTTGTCCGAGGT

GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTTA  
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080  
 CTTCTTTACAGTTGACTCTCCTCGGACTCCTACTGTCAACCGATTGTTCCCAAT

Fig. 8 (cont'd I)

1081 TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT 1140  
 AATTACACAATAATTACCCAACCTAGATTAACCCCTCCCTCTCCAACGTCTCACTCCA  
  
 1141 GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTAGTGTGTCAGTCAGGAA 1200  
 CGTCTCGAACCCACCTGCTACGGTTCCCTATGACTTGGAAATCACACAGGTAGACCTT  
  
 1201 CTGCATCCAATTCAAGGTTCAGTAATGATGTCATTATCCAAACATACCTCTGTAAAATT 1260  
 GACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTTAA

←--- 3.p53-BE ---→  
 (promoter)

1261 CATGCTAAACTACCTAACAGAGCTATCACCGTTCCAAGCAATAGTGACTTGAACAGTGT 1320  
 GTACGATTGATGGATTCTCGATAGATGGCAAGGTTCGTTATCACTGAAACTTGTACACA  
  
 1321 TCACCAAGGACAGGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAATAAT 1380  
 AGTGGTCTCGTCTTCTTAATGTTCTAAAAAAATTCTTTAACCGGTCTTATTAA  
  
 1381 GAGTAACGAAGGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCCATTG 1440  
 CTCATTGCTTCTGCTTCATTAACACTTACAAATTATATCGACCCCCGATACGCTAAC  
  
 1441 GCTTAAGTTGTTAGCTTGTGAGAAATAAAACTAAGGGGCCCTCCCTTT 1500  
 CGAATTCAACAATCGAAACAAAAGGAGAACTCTTATTTGATTCCCCGGGAGGGAAAA  
  
 1501 CAGAGCCCTATGGCGCAACATCTGACTTTCATATGGTTAATGTCCATTCCAGGAAC 1560  
 GTCTCGGGATACCGCGTTGAGACATGAAAAGTATACCAATTGACAGGTAAAGGTCTTG  
  
 1561 GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCCAGTCAAATGCCCGCAAG 1620  
 CAGACACTCGGAGAGTACAACGTCGGTGTGACCTGTCGGTCAGTTACGGGGCGTTC  
  
 1621 TCTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGC 1680  
 AGAAAGAGACTCACTGAGGTGTTAACGTTCCGAGGACATGGTCCGTGGAGACG  
  
 1681 GCTCTGAGCTCCATTCTCTTCAAGACCTCCCCAACTTCCCAGGTTGAACATACGAGAA 1740  
 CGAGACTCGAGGTAAAGAGGAAGTTCTGGAGGGTTGAAGGGTCCAACTTGATGTCGTCTT  
  
 1741 GCCTTAGAAAGGGCAGGAGGCCGGCTCTGAGGTCTCACCTGAAGTGAGCATGCCAGC 1800  
 CGGAAATCTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCG  
  
 1801 CACTGCAGGAACGCCCGGGACAGGAATGCCATTGTGCAACGAACCCGTACTCCTTCC 1860  
 GTGACGTCTTGCGGGGCCCTGTCCTTACGGGTAAACACGTTGCTGGACTGAGGAAGG  
  
 1861 TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC 1920  
 AGTGGGACTGAAGAGGGAGGGATGGCGCGTCCGGTCAACGACTTAGTTACCTCG

Fig. 8 (cont'd II)

CCTCCCCAACCGGGCGTCCCCAGCGAGGCTTCTTCCCATCCTCTGACCACCAGGGGC  
 1921 -----+-----+-----+-----+-----+-----+ 1980  
 GGAGGGGTTGGGCCCGCAAGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG  
  
 TTTCTGTAGCTCGTCTGTGATCTCGCGCAAGAGTGACACACAGGTGTCAAAGACGCTT  
 1981 -----+-----+-----+-----+-----+-----+ 2040  
 AAAAGCACTCGAGCAGAGACTAGAGCGCCTCTCACTGTGTGTCACAAAGTTCTGCGAA  
  
 CTGGGGAGTGAGGGAAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGCACTG  
 2041 -----+-----+-----+-----+-----+-----+ 2100  
 GACCCCTCACTCCCTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCCGTGAC  
  
 GCACGGAAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGGCGAGCTGCCCTTCTCCGC  
 2101 -----+-----+-----+-----+-----+-----+ 2160  
 CGTGCCTTGTGTGGACTCCGGTCGGGACCGACGGGTCCGCCCTGACGGAGAAGAGGGCG  
  
 GCACATGTACAGAGCTCGAGAAAGTACTAGTGGCACGTGGCCGTGACCTTAAGCTTA  
 2161 -----+-----+-----+-----+-----+-----+ 2220  
 CCTGTACATGTCTCGAGCTCTCATGATCACCGGTGCACCCGGCACGTGGAATTGAAAT

←---4.p53-BE---  
(intron)

GGGTCGCTGGAGGGGACCCCGGTTGGAGAGAGGGAGCGGAACCTGGACAGCCCTGAC  
 2221 -----+-----+-----+-----+-----+-----+ 2280  
 CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCGCCTTGAGGACCTGTTGGGACTG

→

AAGCCAAGCAAAGGTCCGCTCCGGCGGGTGGGTGAGTGCAGGCCGCCGGGGCGGGGGC  
 2281 -----+-----+-----+-----+-----+-----+ 2340  
 TTGGTTGGTTCCAGGCAGGCCGCCACCCACTCACGCCGGGGCGCCCCCG  
  
 GGGGAGAGAGCCTGCAGCCTCAGAACAGATATTGCTCATTTCTGGCAGTTCTCAGACG  
 2341 -----+-----+-----+-----+-----+-----+ 2400  
 CCCCTCTCTGGACGTGGAAAGTCTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC  
  
 TAGGAAATAAGTCAGCACCGAACGAGTGGTAAGCCGGAGGGCTCGGAAGAACGGCACCT  
 2401 -----+-----+-----+-----+-----+-----+ 2460  
 ATCCCTTATTCAAGTCGTGGCTCGTCACCAATTGGCCTCCGAGCCTTGTGCCGTGGA  
  
 TTTCTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTACCGTT  
 2461 -----+-----+-----+-----+-----+-----+ 2520  
 AAAGAAAGAGCTTTCAATATACCCCCGACTTACTCGAACGACTCCGAACAAATGGCAA  
  
 TTTTATTGTACACAGAAAAGGAAACTGCCTTGTCTCCCTCCGGAAATTCTCTCTTAA  
 2521 -----+-----+-----+-----+-----+-----+ 2580  
 AAAATAACAGTGTGTCTTCCTTGACGGAACAGAGGGAGGGCTTAAGAGAGAAATT  
  
 GACTGTAAGTCGCTGCCTGAGTGGTTCTGGTCTTCTGCCCTCTCTTCT  
 2581 -----+-----+-----+-----+-----+-----+ 2640  
 CTGACATTCAAGCGACGGACTCACCAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA  
  
 TCTTTGCCCTTCTTAGCTGCACCTCCATGGTGAATTCTGCTGGTCTCTGCTGGGG  
 2641 -----+-----+-----+-----+-----+-----+ 2700  
 AGAAAACGGGAAAGAACGTGAGGGTACCAACTAAAGACGAACCAGAGGACGACCCC

Fig. 8 (cont'd III)

2701 TTGGTGGTACTCGTCCCCACCGCACAGAACCCGGCGCTATTATTGGCCAAGAAACTTGA 2760  
AACCACCATGAGCAAGGGTGGCGTCTGGGCCGCGATAATAACCGGTTCTTGAACT

2761 GCAGCCTGTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAG 2820  
CGTCGGACAAACTTTCAAGGGAGCGAGTCTTACGGTCGAACGTCTACCGATTAGTTTC

2821 AGACGTG 2827  
TCTGCAC

12/26

Fig. 9

<---- 1.p53-BE --

TGAGGACTCTAGGAATATGCTGGTAAAATAACCTT**TAGAGATGCCAACTGT**  
1 -----+-----+-----+-----+-----+-----+ 60  
ACTCCTGAGAGTCCTATACGACCATTATTTATTGGAAATCTACGGGTTGACA  
  
-->  
  
TTTCCCCAGAACACCAGCATTCAATTAGGTGTTCAATTCAATAGATTCTCAAAGGATTCCA  
61 -----+-----+-----+-----+-----+-----+ 120  
AAAGGGGTCTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCTAAGGT  
  
AAGGCAAAGAAGTTGGGAACAGTATATATAATTACCAACCCTTGACATTAGCATA  
121 -----+-----+-----+-----+-----+-----+ 180  
TTCCGTTCTCAAACCCCTGTATATATAATTAAATGGGTTGGGAAACTGTAATCGTATG  
  
TAAGGGCCCTGAGAAGTTGGATTAAGAAAGTTCAAATTAAAGTAACCCAGAATT  
181 -----+-----+-----+-----+-----+-----+ 240  
ATTCCCAGGACTCTCAAAACCTAATTCTTCAAAGTTAATTCAATTGGGCTTAAAA  
  
CTAAGATTATTGACCATGAAACATATGTCCTCCCACAAAGCACATATTCTATCTCCT  
241 -----+-----+-----+-----+-----+-----+ 300  
GATTCTAATAAAACTGGTACTTTGTATACAGAGGGGTGTTCGTGTAAAGGATAGAGGAA  
  
GAACTTGAGGATAATTAGACGTACGTGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA  
301 -----+-----+-----+-----+-----+-----+ 360  
CTTGAACTCCTATTAAATCGCATGCACCCATCTCCATCCCCCTCCCCATACCGTATCT  
  
AAGAGCAGGACCTGGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATTA  
361 -----+-----+-----+-----+-----+-----+ 420  
TTCTCGTCCTGGAACCCCTCGTTATAGATTCAAATTAAAGGACTGAGACGATAAATAAT

<---- 2.p53-BE ---->

ACTAACCATTTGCCAATGTTGCTTAAGCTTTGGCTACATTTTTATTGTAAAG  
421 -----+-----+-----+-----+-----+-----+ 480  
TGATTGGTAGAAACGGTACAACGAATTCAACGAAAAACCGATGTAACAAACATTTC  
  
TAAGTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAAGTAAGGAAGATC  
481 -----+-----+-----+-----+-----+-----+ 540  
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCAATTCAATTCTCTAG  
  
CACATATGTGAGTTGCTGGCTATAATTCAACTCAAGAGATACTGATTTGTCAATTGT  
541 -----+-----+-----+-----+-----+-----+ 600  
GTGTATACACTCAACGACCGAATTAAAGTGTGAGTTCTCTATGACTAAACAGTTAAC  
  
CCTTCCCCCTTTCTCTTCCCTCCTCATTCCCTTACCTCTCCCTTC  
601 -----+-----+-----+-----+-----+-----+ 660  
GGAAAGGGAAAAAGAGAGAAGGGAGGAAGGTAAAGGAAGGAATGGAGAGGAAAG

Fig. 9 (cont'd !)

661 CTTCCCTCACACCCCTTCCTTACATTTTATTTAAATGAACCTTTC  
 661 -----+-----+-----+-----+-----+-----+ 720  
 661 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGAAAAAATAATTACTGAAAAG  
  
 721 ATTTGGAATAGTTAGGATTCAAAAATTGCAAGAGATAATACAGAGAATGCCATA  
 721 -----+-----+-----+-----+-----+-----+ 780  
 721 TAAAACCTTATCAAATCTAAAGTTTAAACGTCTATTATGTCCTACGGGTAT  
  
 781 TACCATCCTCCTTATCCCACCTCTTTGTGTCTATTAGATGCTCAAGAGTGTGCACAA  
 781 -----+-----+-----+-----+-----+-----+ 840  
 781 ATGGTAGGAGGAATAGGGTGAAGAAAACACAGATAATCTACGAGTCTCACACACGTGTT  
  
 841 GGCTGGCACGCCAGGGCTTCCTCATGGCACTAACAGTCACTGAAAGGTGGAACAGAG  
 841 -----+-----+-----+-----+-----+-----+ 900  
 841 CCGACCGTGCAGGTCCCAGAAGGAGTACCGTATTGTCAAGATGACTTCCACCTGTCTC  
  
 901 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG  
 901 -----+-----+-----+-----+-----+-----+ 960  
 901 TGTCGGATAGTGTGGATGTTCTGACCACCATTACGTCACTGTCAGTGTCC  
  
 991 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCA  
 991 -----+-----+-----+-----+-----+-----+ 1020  
 991 CACTACCTTCAGGGACTCCTCCATTGGATTGATCTAAACTCCGGTTGTCCGAGGT  
  
 1021 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTTA  
 1021 -----+-----+-----+-----+-----+-----+ 1080  
 1021 CTTCTTTACAGTTGACTCTCCTCGACTTCCTACTTGTCAACCGATTGTTCCAAAT  
  
 1081 TTAATGTGTTATTAATGGGTGAATCTAATTGGAAAGGGAGAGAGGTTGCAGAGTGAGGT  
 1081 -----+-----+-----+-----+-----+-----+ 1140  
 1081 AATTACACAATAATTACCCAACCTAGATTAACCCCTCCCTCTCCAACGTCTCACTCCA  
  
 1141 GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTACTGTTGTCAGTCTGGAA  
 1141 -----+-----+-----+-----+-----+-----+ 1200  
 1141 CGTCTCGAACCCACCTGCTACGGTTCTTATGACTTGGAAATCACACAGGTACACCTT  
  
 1201 CTGCATCCAAATTCAAGGTTCAAGTCACTACAGTAATAGTTGATGTCATTATCCAAACATACTTCTGTAAAATT  
 1201 -----+-----+-----+-----+-----+-----+ 1260  
 1201 GACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGATGGAAGACATTAA

## &lt;---- 3.p53-BE ----&gt;

1261 CATGCTAAACTACCTAACAGAGCTATCTACCGTTCAAAGCAATAGTGACTTGAACAGTGT  
 1261 -----+-----+-----+-----+-----+-----+ 1320  
 1261 GTACGATTGATGGATTCTCGATAGATGGCAAGGTTCTGTTACTGAAACTTGTACA  
  
 1321 TCACCAAGACGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAAATAAT  
 1321 -----+-----+-----+-----+-----+-----+ 1380  
 1321 AGTGGTCTCGTCTTCTTAATGTTCTAAAAAAATTCTTTAACCGGTCTTATTAA  
  
 1381 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTG  
 1381 -----+-----+-----+-----+-----+-----+ 1440  
 1381 CTCATTGCTCCTGCTCTTACAAACTTACAAATTATCGACCCGATACGCTAAAC  
  
 1441 GCTTAAGTTGTTAGCTTCTTCTTGAGAAATAAAAACATAAGGGCCCTCCCTTT  
 1441 -----+-----+-----+-----+-----+-----+ 1500  
 1441 CGAATTCAACAAATCGAAACAAAGGAGAACTCTTATTTGATTCCCCGGAGGGAAAA  
  
 1501 CAGAGCCCTATGGCGAACATCTGACTTTCTATGGTAACGTCCATTCCAGGAAC  
 1501 -----+-----+-----+-----+-----+-----+ 1560  
 1501 GTCTCGGGATACCGCGTTGAGACATGAAAAGTATACCAATTGACAGGTAAAGTCCTG

Fig. 9 (cont'd II)

1561 GTCGTGAGCTCTCATGTTGCAGCCACAACATGGACAGCCCAGTCAAATGCCCGCAAG 1620  
 CAGACACTCGGAGAGTACAACGTCGGTGTACCTGTCGGTCAGTTACGGGGGTTC

1621 TCTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC 1680  
 AGAAAGAGACTCACTGAGGTCGTTAACGTTCCGAGGACATGGTCCTGGAGACG

1681 GCTCTGAGCTCCATTCTCCTCAAGACCTCCCCAACTTCCAGGTTGAACACAGCAGAA 1740  
 CGAGACTCGAGGTAAGAGGAAGTCTGGAGGGTTGAAGGGTCCAACTTGATGTCGTCTT

1741 GCCTTAGAAAAGGGCAGGAGGCCGGCTCTGAGGTCTCACCTGAAGTGAGCATGCCAGC 1800  
 CGGAAATCTTCCCCTCCGGCCAGAGCTCCAGGAGTGGACTTCACGTACGGTCG

1801 CACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTCAACGAACCTGACTCCTCC 1860  
 GTGACGTCTTGCGGGGCCCTGTCCTACGGTAAACACGTTGCTTGGACTGAGGAAGG

1861 TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC 1920  
 AGTGGGACTGAAGAGGGGGAGGGATGGCGCGTCCGGTCAACGACTTAGTTACCTCG

1921 CCTCCCCAACCGGGCGTCCCCAGCGAGGCTCCTCCATCCTGACCACCGGGGC 1980  
 GGAGGGGTTGGGCCCGCAAGGGGTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG

1981 TTTCGTGAGCTCGTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT 2040  
 AAAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCACAAGTTCTGCGAA

2041 CTGGGGAGTGAGGGAAAGCGGTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGCACTG 2100  
 GACCCCTCACTCCCTCGCAAATGCTCACTGAACCGACCTCGGAGTCCCCTCGTGA

2101 GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCCAGCTGCCCTTCTCCGC 2160  
 CGTGCCTTGTGTGGACTCCGGTCGGACCGACGGTCCGCTCGACGGAGAACAGGGCG

2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCACGTGGCCGTGACCTTAAGCTTA 2220  
 CCTGTACATGTCTCGAGCTTCAATGATCACCGGTGCACCCGGCACGTGGAATTGAAAT

<---- 4.p53-BE  
(intron)

2221 GGGTCGCTGGAGGGGACCCCGGTTGGAGAGAGGGAGCGGAACCTCTGGACAAAGCCCTGAC 2280  
 CCCAGCGACCTCCCCCTGGGCCAACCTCTCTCCTCGCCTGAGGACCTGTTGGGACTG

----->

2281 AAGCCAAGCAAAGGTCCGCTCCGGCGGGTGGTGAGTGCGCGCCGCCCCGGGGGC 2340  
 TTCCGGTTCGGTTCCAGGCGAGGCCGCCACCCACTCACGCGCGCCGGGGCGCCCCCG

2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTCTGGCAGTTCTCAGACG 2400  
 CCCCTCTCGGACGTGGAAAGTCTGTCTAACGAGTAAAGACCGTCAAGAGTCTGC

Fig. 9 (cont'd III)

TAGGAAATAAGTCAGCACCGAACAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT  
 2401 -----+-----+-----+-----+-----+-----+ 2460  
 ATCCTTATTCACTCGTGGCTTCGTACCAATTCCGGCTCCCGAGCCTTGTGCCGTGGA  
  
 TTTCTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTCTGGAGGCTTGTACCGTT  
 2461 -----+-----+-----+-----+-----+-----+ 2520  
 AAAGAAAGAGCTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA  
  
 TTTTATTGTACACAGAAAAGGAAACTGCCTTGCTCCCTCCGGAAATTCTCTTTAA  
 2521 -----+-----+-----+-----+-----+-----+ 2580  
 AAAATAACAGTGTGTCTTTCTTGACGGAACAGAGGGAGGGCTTAAGAGAGAAATT  
  
 GACTGTAAGTCGCTGCCTGAGTGGTTCACTTGTGTTCTGCCCTCTCTTTCT  
 2581 -----+-----+-----+-----+-----+-----+ 2640  
 CTGACATTCAAGCGACGGACTCACCAAGTAAAACAAAACAAAAGACGGGAAGAGAAAGA  
  
 TCTTTGCCCTTCTTAGCTTGCACCTCCATGGTATTCTGCTGGTCTCCTGCTGGGG  
 2641 -----+-----+-----+-----+-----+-----+ 2700  
 AGAAAAACGGAAAGAACGAAACGTGAGGGTACCAACTAAAGACGAACCAAGAGGAGACCCC  
  
 TTGGTGGTACTCGTCCCACCGCACAGAACCCGGCGCTATTATTGCCAAGAAACTTGA  
 2701 -----+-----+-----+-----+-----+-----+ 2760  
 AACCAACATGAGCAAGGGTGGCGTGTCTGGGCCGGATAATAACCGTTCTTGAAC  
  
 GCAGCCTGTTTGAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAG  
 2761 -----+-----+-----+-----+-----+-----+ 2820  
 CGTCGGACAAAACCTTCAAGGGAGCGAGTCTTACGGTCAACGTCTACCGATTAGTTTC  
  
 AGACGTG  
 2821 ----- 2827  
 TCTGCAC

010234567890 010234567890 010234567890 010234567890

Fig. 10

<---- 1.p53-BE ----  
(promoter)

1 TGAGGACTCTAGGAATATGCTGGAAAATAACCTTAGAGATGCCAAACTGT 60  
 1 ACTCCTGAGAGTCCTTATACGACCATTATTTTATTGAAATCTCTACGGGTTGACA  
 -->  
 61 TTTCCCCAGAACACCAGCATTCAATTAGGTGTTCAATAGATTCTCAAAGGATTCCA 120  
 61 AAAGGGGTCTTGTGGTCGAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCCCTAAGGT  
 121 AAGGCAAAGAAGTTGGGAACAGTATATATAATTACCCAAACCTTGACATTAGCATA 180  
 121 TTCCGTTCTCAAACCCCTGTCAATATATTAATGGGTTGGGAAACTGTAATCGTATG  
 181 TAAGGGCCCTGAGAAGTTGGATTAAAGAAAGTTCAAAATTAAAGTAACCCAGAATT 240  
 181 ATTCCCGGGACTCTCAAACCTAATTCTTCAAAGTTAATTCAATTGGGCTTAAAA  
 241 CTAAGATTATTGACCATGAAACATATGTCCTCCCACAAAGCACATATTCCATCTCCTT 300  
 241 GATTCTAATAAACTGGTACTTGTATACAGAGGGGTGTTCGTGTATAAGGATAGAGGAA  
 301 GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA 360  
 301 CTTGAACCTCTATTAATCTGCATGCACCCATCTCCATCCCCTCCCCATACCGTATCT  
 361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATTA 420  
 361 TTCTCGTCTGGAACCCCTCGTTCTATAGATTCAAATTAGGACTGAGACGATAATAAT

<---- 2.p53-BE ---->  
(promoter)

421 ACTAACCATTTGCCAATGTTGCTTAAGCTTTGGCTACATTTTTATTGTAAAG 480  
 421 TGATTGGTAGAAACGGTTACAACGAATTGAAAAACCGATGTAAAAAAAACATTTC  
 481 TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540  
 481 ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCTAATTCTCTCTAG  
 541 CACATATGTGAGTTGCTGGCTATAATTACACTCAAGAGATACTGATTTGTCATTGT 600  
 541 GTGTATACACTCAACGACCGAATATTAAAGTGTGAGTTCTATGACTAAAACAGTTAAC  
 601 CCTTCCCCTTTTCTCTCTTCCCTCCATTCTTACCTCTTACCTCTCCTTC 660  
 601 GGAAAGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGATGGAGAGGAAAG  
 661 CTTCCCTCACACCCCTTCCCTCTTACATTAAATTAAATGAACTTTTC 720  
 661 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAATAATTACTTGAAAAG  
 721 ATTTGGAATAGTTAGGATTCAAAATTTGCAAGAGATAATACAGAGAATGCCATA 780  
 721 TAAACCTTATCAAAATCTAAAGTTAAACGTCTATTATGCTCTACGGGTAT

Fig. 10 (cont'd I)

781 TACCATCCTCCTTATCCCACCTCTTTGTCTATTAGATGCTCAGAGTGTGACAA 840  
 ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT  
  
 841 GGCTGGCACGCCAGGGTCTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG 900  
 CCGACCGTGCGGTCCCAGAAGGAGTACCGTGATTGTCAAGATGACTTCCACACTGTCTC  
  
 901 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG 960  
 TGTTCGGATAGTTGTGGATGTTCTGACCACCATCAGTCAGTCTACGTTGTGTC  
  
 961 GTGATGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAACAGGCTCAG 1020  
 CACTACCTTCGGGAGTCCTCCATTGGATTGGATCTAAACTCCGGTTGTCCGAGGTC  
  
 1021 AAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTTAT 1080  
 TTCTTTACAGTTGACTCTCCTCGGACTTCTACTTGTCAACCGATTGTTCCAATA  
  
 1081 TAATGTGTTATAATGGGTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGTG 1140  
 ATTACACAATAATTACCCAACCTAGATTAACCCCTCCCTCTCCAACGTCTACTCCAC  
  
 1141 CAGAGCTTGGTGGACGATGCCAAGGAATACTGAAACCTTGTGTCCAGTCAGGAAAC 1200  
 GTCTCGAACCCACCTGCTACGGTTCTTATGACTTGGAAATCACACAGGTCAAGACCTTG  
  
 1201 TGCACTCAAATTCAAGGTTAGTAATGATGTCATTATCAAACATAACCTCTGTAAAATT 1260  
 ACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTTAAG  
  
 <---- 3.p53-BE ---->  
 (promoter)

1261 ATGCTAAACTACCTAACAGAGCTATCTACCGTTCAAAGCAATAGTGAACAGTGT 1320  
 TACGATTGATGGATTCTCGATAGATGGCAAGGTTCTGTATCACTGAAACTGTCACAA  
  
 1321 CACCAAGCAGCAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAATAATG 1380  
 GTGGTCTCGTCTTCTTAATGTTCTAAAAAAATTCTTTAACCGGTCTTATTAC  
  
 1381 AGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTGG 1440  
 TCATTGCTTCTGTCTTCATTAACACTACAAATTATATCGACCCCGATACGCTAAACC  
  
 1441 CTTAAGTTGTTAGCTTGTCTCTTGAGAAAATAAAACTAAGGGCCCTCCCTTTC 1500  
 GAATTCAACAAATCGAAACAAAAGGAGAACTCTTATTTGATTCCCGGGAGGGAAAAG  
  
 1501 AGAGCCTATGGCGAACATCTGTACTTTCATATGGTTAATGTCCATTCCAGAAACG 1560  
 TCTCGGAATACCGCGTTGAGACATGAAAAGTATACCAATTGACAGGTAAAGGTCTTGC  
  
 1561 TCTGTGAGCCTCTCATGTTGAGCCACAACATGGACAGGCCAGTCAGTCAAATGCCCGCAAGT 1620  
 AGACACTCGGAGAGTACAACGTCGGTGTACCTGTCGGGTCAAGTTACGGGGCGTTCA  
  
 1621 CTTCTCTGAGTGAATCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGCG 1680  
 GAAAGAGACTCACTGAGGTCGTTAATCGGTTCCAGGACATGGTCGGTCTGGAGACGC  
  
 1681 CTCGAGCTCATTCTCCTCAAGACCTCCCCACTTCCAGGTTGAACATACAGCAGAAG 1740  
 GAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTGAAGGGTCAACTTGTGTCGTCTTC

Fig. 10 (cont'd II)

1741 CCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCTCACCTGAAGTGAGCATGCCAGCC  
 1801 GGAAATCTTCCCGTCCTCCGGCCGAGAGCTCAGGAGTGGACTTCACTCGTACGGTCGG  
 1861 ACTGCAGGAACGCCCGGGACAGGAATGCCATTGTCAACGAACCTGACTCCTCCT  
 1861 TGACGTCTTGCAGGGCCCTGTCTTACGGTAAACACGTGCTTGGACTGAGGAAGGA  
 1921 CACCTGACTTCTCCCCCTCCCTACCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC  
 1921 GTGGGACTGAAGAGGGGAGGGATGGCGCGTCCGGTCAACGACTTAGTTACCTCGG  
 1981 CTCCCCAACCGGGCGTCCCCAGCGAGGCTTCTCCATCCTGACCACCGGGCT  
 1981 GAGGGGTTGGGCCCGCAAGGGTGCCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCGA  
 2041 TTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC  
 2041 AAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTCACAAGTTCTGCGAAG  
 2101 TGGGGAGTGAGGGAAAGCGGTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGACTGG  
 2101 ACCCTCACTCCCTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCAGCCGTGACC  
 2161 CACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCCAGCTGCCCTTCTCCCG  
 2161 GTGCCTTGTGAGGGACTCCGGTCCGGACCGACGGGTCGCCCTCGACGGAGAAGAGGGCGC  
 2221 GGTGGTGGACCCGCTCAGTACGGAGTTGGGAAAGCTTTCACTTGGAGGATTGCTCA  
 2221 CCAACCACCTGGCGAGTCATGCCCTCAACCCCTTCGAGAAAGTGAAGCCTCTAACGAGT  
 2281 ACAACCATGCTGGCATCTGGACCCCTTACCTCTGGTGAATCCCTCTCTGCCCGGGTGG  
 2281 TGTGGTACGACCGTAGACCTGGAGGATGGAGACCACTAGGGAGAGGACGGGCCACC  
 2341 AGGCTTACCCCGTCTTAGTCCCGGGATAGGCAAAGTGGGGCGGGCGGGACGGTGC  
 2341 TCCGAATGGGCAGAATCAGGGCCCTATCCGTTCACCCCGCCCGCCCTGCGCACGC  
 2401 GGATTGGCGGGCAGCGGCCACGCCGGCACCTGGAGGCCGGCTGCTGCCGGAGGCG  
 2401 CCTAACGCCCGTGCCTGGCGTGGACCCCTGCCGCCGACGACGCCCTCCGC  
 2461 TTGGAGACTGGCTCCGGGGCTGTTAGGACCTTCCCTAGGCCCGGGTGCTCAGAACGA  
 2461 AACCTCTGACCGAGGGCCCCGACAATCCTGGAAGGGAGTCCGGGCCACGAGTCTTGCT  
 2521 TGGAGGACTTGCTTTCTGGCCTTGATGCGAAGTGCTGATCCCGTGGCAGGCCGGGG  
 2521 ACCCTCTGAACGAAAAGAACCCGAAACTACGCTTACGACTAGGGCGACCGTCCGCC  
 2581 CAGCTCCGGCGCTCTCGGAGGACCAACTGCGCTCCACGTTGAGGTGGCGTGGGGGGCGGA  
 2581 GTCGAGGCCCGAGGAGCCTCTGGTACGCGAGGTGCAACTCCACCCGACCCCCCGCCT  
 2641 CAGGAATTGAAGCGGAAGTCTGGGAAGCTTGGAGGCTGGAGGGGACCCCGTTGGA  
 2641 GTCCTTAACCTCGCCTTCAGACCCCTCGAAATCCCAGCGACCTCCCCCTGGGCCAACCT

&lt;---- 4.p53-BE ----&gt;

(intron)

2641 GAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAAGCCAAAGGTCCGCTCCGGCGC  
 2641 CTCTCCTCGCCTTGAGGACCTGTTGGACTGTTGGTTCCAGGCGAGGCCGCG

Fig. 10 (cont'd III)

2701	GGGTGGGTGAGTGC CGCCGCCGCCGCCGGGGGGAGAGAGCTACAGCCTTCAGAACCA	2760
	CCCACCCACTCACGCGGGCGGGCGCCCCCTCTCGGATGTCGGAAAGTCTTGT	
2761	CATATTGCTCATTTCGGCAGTTCTCAGACGTAGGAATAAGTCAGCACCGAACAGCTG	2820
	GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTATTCACTGGCTTCGTAC	
2821	GTAAAGCCGGAGGGCTCGGAAGAACGGCACCTTTCTCGAAAAAGTTATATGGGGG	2880
	CAATTGGCCTCCCGAGCCTTCTGCCGTGGAAAAGAAAGAGCTTTCAATATAACCCCC	
2881	CTGAATGAGCTTCTGGAGGCTTGTACCGTTTTATTGTACACAGAAAAGGAAACTG	2940
	GACTTACTCGAACGACCTCCGAACAAATGGAAAAATAACAGTGTGTCTTCCTTGAC	
2941	CCTTGTCTCCCTTCCGGGAATTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC	3000
	GGAACAGAGGGAGGCCCTTAAGAGAGAAATTCTGACATTAGCGACGGACTCACCAAAG	
3001	ATTTTGTTTGTTTCTGCCCTCTCTTTCTTTGCCCTTCTTAGCTTGCACCTCC	3060
	TAAAACAAAACAAAAAGACGGGAACAGAGAAAGAAGAAACGGAAAGAACGTGAGG	
3061	CATGGTGATTTCTGCTGGTCTCTGCTGGGGTTGGTGGTACTCGTCCCACCGCACAGA	3120
	GTACCAACTAAAGACGAACCAGAGGGACGACCCCAACCACCATGAGCAAGGGTGGCGTGTCT	
3121	ACCCGGCGCCTATTATTGGCAAGAAACTTGAGCAGCCTGTTTGAAGAGTCCCTCGCTC	3180
	TGGGCCGCGGATAATAACCGGTTCTTGAACTCGTCGGACAAAACCTTCAGGGAGCGAG	
3181	AGAAATGCCAGCTTGAGATGGCTAATCAAAG	3212
	TCTTACGGTCGAACGCTACCGATTAGTTTC	

Fig 11

variations in the p53 binding region of figure 8

### 1. p1140 IMI

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMI	GG <b>A</b> AAGCCCTGACAAGCCA
	↑

positions of the mutations (boldface and arrow): 2270 (C→A)

### 2. p1140 IMII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMII	GG <b>A</b> <b>A</b> AAGCCCTG <b>A</b> <b>A</b> AGCCA
	↑                           ↑

positions of the mutations (boldface and arrow): 2270 (C→A)  
2280 (C→A)

### 3. p1140 IMIII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMIII	GG <b>A</b> <b>A</b> <b>A</b> <b>T</b> CCCTG <b>A</b> <b>A</b> <b>A</b> <b>T</b> CCA
	↑   ↑                   ↑   ↑

positions of the mutations (boldface and arrow): 2270 (C→A)  
2273 (G→T)  
2280 (C→A)  
2283 (G→T)

4. **p1140 IMIV**

p1140                    **GGACAAGCCCTGACAAGCCA**  
p1140 IMIV            **GCACAAGCCCT**CACAAGCCA****  
                          ↑                    ↑

positions of the mutations (boldface and arrow): 2268 (G→T)

2278 (C→A)

Fig. 12

variations in the p53 binding regions of figure 9

### 1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	<b>GGAA</b> <b>AA</b> TCCCTGA <b>AA</b> ATCCA
	↑   ↑                   ↑    ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

p1141 IMIII

### 2. p1141 1p53

p1141	AGAGATGCCAAACTGTTTT
p1141 1p53	<b>AGAGATT</b> CCCAAA <b>AT</b> GTTTT
	↑                   ↑

positions of the mutations (boldface and arrow): 50

57

### 3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTTT
p1141 2p53	<b>AATGTT</b> TCTTAAGATTTTT
	↑                   ↑

positions of the mutations (boldface and arrow): 443

450

## 4. p1141 3p53

p1141                   AAACTACCTAAGAGCTATCT

p1141 3p53           **ACA**ATACCTAAGAGCTATCT

↑↑

positions of the mutations (boldface and arrow): 1268                   (A→C)

1270                   (C→A)

## 5. p1141 ΔBgl

p1141                   AATAACCTTT**AGAGATGCCAAA**CTGTTTCCCCAGAACAA

**p1141ΔBgl**           AATAACCTTTA-----**GATCT**CCCCAGAACAA

## 6. p1141 ΔSpe

p1141                   CATCTTGGCC**AATGTTGCTTAAGCTTTTT**GGCTACATTT

**p1141ΔBgl**           CATCTTGGCC-----**CTAGT**GGCTACATTT

## 7. p1141 ΔMph

p1141                   AATTCA**TGCTAA**ACTACCTAAGAGCTATCTACCGTTCAA

**p1141ΔBgl**           AATTCA**TGCTATGCA**-----TACCGTTCAA

Fig. 13

variations in the p53 binding region of figure 10

### 1. p1142 TAG

mutation of the positions: 2227 (A→T)  
2228 (T→A)

### 2. p1142 IMIII

p1142	GGACAAAGCCCTGACAAGCCA
p1142 IMIII	<b>GGAAAATCCCTGAAATCCA</b> ↑↑↑↑

positions of the mutations (boldface and arrow): 2662 (C→A)  
2665 (G→T)  
2672 (C→A)  
2675 (G→T)

### 3. p1142 ΔBgl

<---- 1.p53-BE ---->	
p1142	AATAACCTT <b>A</b> GAGATGCCAAACTGTTTCCCCAGAACCA
p1142ΔBgl	AATAACCTT <b>A</b> -----GATCTCCCCAGAACCA

### 4. p1142 ΔSpe

<---- 2.p53-BE ---->	
p1142	CATCTTGCC <b>A</b> ATGTTGCT <b>T</b> AAGCTTTGGCTACATTT
p1142ΔBgl	CATCTTGCC <b>A</b> -----CTAGTGGCTACATTT

## 5. p1142 ΔMph

<---- 3.p53-BE ---->

pl142	AATT CAT GCT <b>AAACTACCTAAGAGCTATCTACCGTTCCAA</b>
pl142ΔBgl	AATT CAT GCT <b>TATGCA</b> -----TACCGTTCCAA

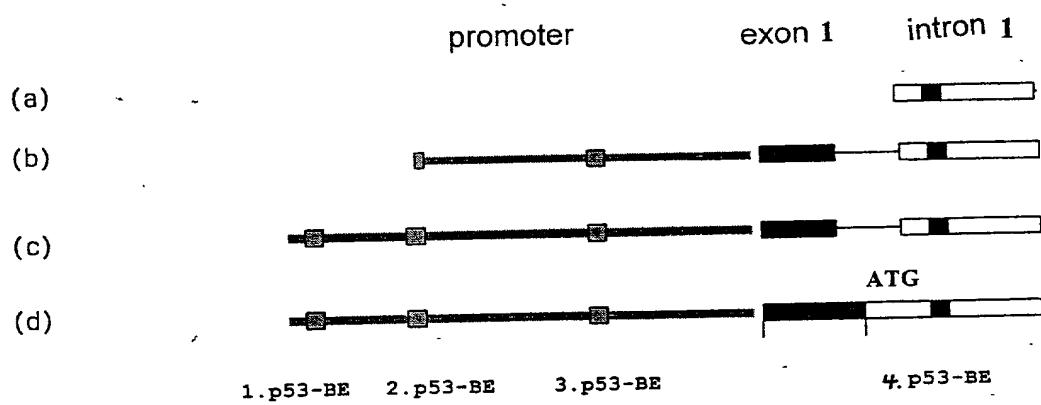


Fig. 14